RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/040,722

DATE: 01/21/2003
TIME: 16:05:24

Input Set : A:\50047.006003.SEQLIST.TXT
Output Set: N:\CRF4\01212003\J040722.raw

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 4  <110> APPLICANT: Ruiz-Opazo, Nelson
 6  <120> TITLE OF INVENTION: METHOD OF ASSAYING MODULATORS OF
        HYPERTENSION
 8  <130> FILE REFERENCE: 50047/006003
11  <140> CURRENT APPLICATION NUMBER: US 10/040,722
12  <141> CURRENT FILING DATE: 2002-01-07
14  <150> PRIOR APPLICATION NUMBER: US 09/653,030
15  <151> PRIOR FILING DATE: 2000-09-01
17  <150> PRIOR APPLICATION NUMBER: US 60/152,011
18  <151> PRIOR FILING DATE: 1999-09-01
20  <160> NUMBER OF SEQ ID NOS: 4
21  <170> SOFTWARE: PatentIn for Windows Version 4.0
24  <210> SEQ ID NO: 1
25  <211> LENGTH: 363?
26  <212> TYPE: DNA
27  <213> ORGANISM: Rattus norvegicus
28  <220> FEATURE:
29  <221> NAME/KEY: CDS
31  <222> LOCATION: (158)...(3093)
32  <400> SEQUENCE: 1
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     ggcggagcgg cgcgcgcgtc ggtcggtgtc gccgggccgtc ctcctctctt cctccggcgg  120
     gacccctagt tccccgcgct cggttcccac ggctccactc tcccagccgg gagctgctct  180
     gtcctcttig tagtctgag ccacaggcgc cggcgcgggg cccgcagcgc cgccacc atg  240
                                                                       Met
                                                                        1
     ggg aag ggg gtg ggg cga gac aag tat gag ccc gca gct gta tca gaa   288
     Gly Lys Gly Val Gly Arg Asp Lys Tyr Glu Pro Ala Ala Val Ser Glu
                  5                    10                   15
     cat ggg gac aag aag atc aag aag gcg aag aag gaa agg gac atg gac   336
     His Gly Asp Lys Lys Ser Lys Lys Ala Lys Lys Glu Arg Asp Met Asp
                 20                   25                    30
     gag ctc aag aag gtg gtg tct atg gac gac cat aaa ctc agc ctg gat   384
     Glu Leu Lys Lys Val Val Ser Met Asp Asp His Lys Leu Ser Leu Asp
             35                   40                    45
     gag ctc cat cgt aaa tac gga aca gat ttg agc cga ggc cta aca ccc   432
     Glu Leu His Arg Lys Tyr Gly Thr Asp Leu Ser Arg Gly Leu Thr Pro
             50                   55                   60               65
     gca agg gcc gct gag atc ctg gct cgg gat ggc ccc aac gcc ctc acg   480
     Ala Arg Ala Ala Glu Ile Leu Ala Arg Asp Gly Pro Asn Ala Leu Thr
                 70                   75                    80
     cca cct ccc act act ccc gag tgg gtc aaa ttc tgt cga cag ctg ttc   528
     Pro Pro Pro Thr Thr Pro Glu Trp Val Lys Phe Cys Arg Gln Leu Phe
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65              85                   90                    95
65 ggt ggc ttc tcc atg tta ctg tgg att gga gcc att ctt tgt ttc ttg    576
66 Gly Gly Phe Ser Met Leu Leu Trp Ile Gly Ala Ile Leu Cys Phe Leu
67          100                   105                   110
69 gct tat ggc atc cga agt gct aca gaa gag gaa cca cca aat gat gat    624
70 Ala Tyr Gly Ile Arg Ser Ala Thr Glu Glu Glu Pro Pro Asn Asp Asp
71          115                   120                   125
73 ctg tac ctc ggg gtc gtg ctg tct gct gtc gtc atc ata act ggc tgt    672
74 Leu Tyr Leu Gly Val Val Leu Ser Ala Val Val Ile Ile Thr Gly Cys
75 130                   135                   140                   145
77 ttc tcc tat tat caa gaa gca aaa agc tcc aag atc atg gaa tcc ttc    720
78 Phe Ser Tyr Tyr Gln Glu Ala Lys Ser Ser Lys Ile Met Glu Ser Phe
79                   150                   155                   160
81 aag aac atg gtc cct cag caa gcc ctc gtg att cga aat gga gag aag    768
82 Lys Asn Met Val Pro Gln Gln Ala Leu Val Ile Arg Asn Gly Glu Lys
83          165                   170                   175
85 atg agc atc aac gca gag gat gtc gtc gtt ggt gat ctg gtg gag gtg    816
86 Met Ser Ile Asn Ala Glu Asp Val Val Val Gly Asp Leu Val Glu Val
87          180                   185                   190
89 aag ggc gga gac cga atc cct gct gat ctc aga atc ata tct gca aat    864
90 Lys Gly Gly Asp Arg Ile Pro Ala Asp Leu Arg Ile Ile Ser Ala Asn
91          195                   200                   205
93 ggc tgc aag gtg gat aac tcc tca ctc act ggt gaa tca gaa ccc cag    912
94 Gly Cys Lys Val Asp Asn Ser Ser Leu Thr Gly Glu Ser Gln Pro Gln
95 210                   215                   220                   225
97 act cgg tcc ccg gat ttc aca aac gag aac ccc ttg gag aca agg aac    960
98 Thr Arg Ser Pro Asp Phe Thr Asn Glu Asn Pro Leu Glu Thr Arg Asn
99                   230                   235                   240
101 att gcc ttc ttc tca acc aac tgt gtt gaa gga act gca cgt ggc atc    1008
102 Ile Ala Phe Phe Ser Thr Asn Cys Val Glu Gly Thr Ala Arg Gly Ile
103          245                   250                   255
105 gtt gtg tac act ggg gat cgc acc gtg atg ggc agg atc gcc acc ctt    1056
106 Val Val Tyr Thr Gly Asp Arg Thr Val Met Gly Arg Ile Ala Thr Leu
107          260                   265                   270
109 gct tct ggg ctg gaa ggc ggc cag acc ccc att gct gaa gaa atc gag    1104
110 Ala Ser Gly Leu Glu Gly Gly Gln Thr Pro Ile Ala Glu Glu Ile Glu
111          275                   280                   285
113 cac ttc atc cac ctc atc acg ggt gtg gcc gtg ttc ctg ggg gtg tct    1152
114 His Phe Ile His Leu Ile Thr Gly Val Ala Val Phe Leu Gly Val Ser
115 290                   295                   300                   305
117 ttc ttc att ctc tct ctg atc ctt gag tac acc tgg ctc gag gct gtc    1200
118 Phe Phe Ile Leu Ser Leu Ile Leu Glu Tyr Thr Trp Leu Glu Ala Val
119                   310                   315                   320
121 atc ttc ctc att ggt atc atc gta gcc aac gtg ccc gaa ggt ttg ctg    1248
122 Ile Phe Leu Ile Gly Ile Ile Val Ala Asn Val Pro Glu Gly Leu Leu
123                   325                   330                   335
125 gcc acc gtc acg gta tgt ctg acg ctc act gcc aag cgc atg gcg agg    1296
126 Ala Thr Val Thr Val Cys Leu Thr Leu Thr Ala Lys Arg Met Ala Arg
127          340                   345                   350
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129  aag aac tgc ctg gtg aag aac ctg gaa gct gtg gag acc ttg ggg tcc    1344
130  Lys Asn Cys Leu Val Lys Asn Leu Glu Ala Val Glu Thr Leu Gly Ser
131      355                 360                 365

133  aca tcc acc atc tgc tcc gac aag act gga act ctg act cag aac cgg    1392
134  Thr Ser Thr Ile Cys Ser Asp Lys Thr Gly Thr Leu Thr Gln Asn Arg
135  370                 375                 380                 385

137  atg aca gtg gct cac atg tgg ttt gac aat caa atc cat gaa gct gac    1440
138  Met Thr Val Ala His Met Trp Phe Asp Asn Gln Ile His Glu Ala Asp
139                  390                 395                 400

141  acc aca gag aat cag agt ggg gtc tcc ttt gac aag acg tca gcc acc    1488
142  Thr Thr Glu Asn Gln Ser Gly Val Ser Phe Asp Lys Thr Ser Ala Thr
143                  405                 410                 415

145  tgg ttc gct ctg tcc aga att gct ggg ctc tgt aac agg gca gtg ttt    1536
146  Trp Phe Ala Leu Ser Arg Ile Ala Gly Leu Cys Asn Arg Ala Val Phe
147      420                 425                 430

149  cag gct aac caa gaa aac ctg cct atc ctt aag cgt gca gta gcg gga    1584
150  Gln Ala Asn Gln Glu Asn Leu Pro Ile Leu Lys Arg Ala Val Ala Gly
151      435                 440                 445

153  gat gct tcc gag tcg gcg ctc tta aag tgc atc gag gtc tgc tgt ggc    1632
154  Asp Ala Ser Glu Ser Ala Leu Leu Lys Cys Ile Glu Val Cys Cys Gly
155  450                 455                 460                 465

157  tcc gtg atg gag atg agg gag aac tac acc aag ata gtg gag att cct    1680
158  Ser Val Met Glu Met Arg Glu Lys Tyr Thr Lys Ile Val Glu Ile Pro
159                  470                 475                 480

161  ttc aac tcc acc aac aag tac cag ctc tcc att cac aag aac cca aat    1728
162  Phe Asn Ser Thr Asn Lys Tyr Gln Leu Ser Ile His Lys Asn Pro Asn
163                  485                 490                 495

165  gca tcg gag ccc aag cac ctg cta gtt atg aag ggc gcc cca gaa aga    1776
166  Ala Ser Glu Pro Lys His Leu Leu Val Met Lys Gly Ala Pro Glu Arg
167      500                 505                 510

169  atc ctg gac cga tgc agt tct atc ctc ctc cac ggc aag gag cag ccc    1824
170  Ile Leu Asp Arg Cys Ser Ser Ile Leu Leu His Gly Lys Glu Gln Pro
171      515                 520                 525

173  ctg gac gaa gag ctg aag gac gcc ttt cag aat gct tac cta gag ctg    1872
174  Leu Asp Glu Glu Leu Lys Asp Ala Phe Gln Asn Ala Tyr Leu Glu Leu
175  530                 535                 540                 545

177  ggt ggc ctt gga gag cgt gtg cta ggt ttc tgc cac ctc ctt ctg cct    1920
178  Gly Gly Leu Gly Glu Arg Val Leu Gly Phe Cys His Leu Leu Leu Pro
179                  550                 555                 560

181  gat gaa cag ttt ccc gaa ggc ttc cag ttt gac act gat gaa gtc aat    1968
182  Asp Glu Gln Phe Pro Glu Gly Phe Gln Phe Asp Thr Asp Glu Val Asn
183                  565                 570                 575

185  ttc ccc gtg gat aac ctc tgc ttc gtg ggt ctt atc tcc atg att gac    2016
186  Phe Pro Val Asp Asn Leu Cys Phe Val Gly Leu Ile Ser Met Ile Asp
187                  580                 585                 590

189  cct cct cga gct gct gtc ccc gat gct gtg ggg aaa tgc cgc agc gct    2064
190  Pro Pro Arg Ala Ala Val Pro Asp Ala Val Gly Lys Cys Arg Ser Ala
191      595                 600                 605

193  ggg att aag gtc atc atg gtc aca gga gac cat cca atc aca gcc aaa    2112
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194 Gly Ile Lys Val Ile Met Val Thr Gly Asp His Pro Ile Thr Ala Lys
195 610                 615                 620                 625
197 gcc att gct aag ggg gtg ggc att atc tca gaa ggt aac gag acc gtc   2160
198 Ala Ile Ala Lys Gly Val Gly Ile Ile Ser Glu Gly Asn Glu Thr Val
199                 630                 635                 640
201 gaa gac att gct gcc cgc ctc aac att cca gtg aac cag gtg aac ccc   2208
202 Glu Asp Ile Ala Ala Arg Leu Asn Ile Pro Val Asn Gln Val Asn Pro
203                 645                 650                 655
205 aga gat gcc aag gcc tgt gta gta cat ggc agt gac ttg aag gac atc   2256
206 Arg Asp Ala Lys Ala Cys Val Val His Gly Ser Asp Leu Lys Asp Met
207                 660                 665                 670
209 acc tct gag gag ctg gat gac att ttg cgt tac cac acg gag att gtc   2304
211 Thr Ser Glu Glu Leu Asp Asp Ile Leu Arg Tyr His Thr Glu Ile Val
211     675                 680                 685
213 ttt gct agg acc tct cct caa cag aag ctt atc att gtg gag ggt tgc   2352
214 Phe Ala Arg Thr Ser Pro Gln Gln Lys Leu Ile Ile Val Glu Gly Cys
215 690                 695                 700                 705
217 caa cgg cag ggt gcc atc gtg gct gtc aca ggg gat ggt gtc aat gac   2400
218 Gln Arg Gln Gly Ala Ile Val Ala Val Thr Gly Asp Gly Val Asn Asp
219                 710                 715                 720
221 tct cca gct ttg aaa aag gca gat att gga gtt gcc atg ggg att gtt   2448
222 Ser Pro Ala Leu Lys Lys Ala Asp Ile Gly Val Ala Met Gly Ile Val
223                 725                 730                 735
225 ggc tcg gat gtg tcc aag caa gct gct gac atg att ctt ctg gat gac   2496
226 Gly Ser Asp Val Ser Lys Gln Ala Ala Asp Met Ile Leu Leu Asp Asp
227                 740                 745                 750
229 aac ttt gcc tcc atc gtt act gga gta gaa gaa ggt cgt ctg ata ttt   2544
230 Asn Phe Ala Ser Ile Val Thr Gly Val Glu Glu Gly Arg Leu Ile Phe
231     755                 760                 765
233 gat aac ttg aag aaa tcc att gct tac acc cta aca agt aac att cca   2592
234 Asp Asn Leu Lys Lys Ser Ile Ala Tyr Thr Leu Thr Ser Asn Ile Pro
235     770                 775                 780                 785
237 gaa atc acc ccc ttc ttg ata ttt att att gca aac atc cca ctt ccc   2640
238 Glu Ile Thr Pro Phe Leu Ile Phe Ile Ile Ala Asn Ile Pro Leu Pro
239                 790                 795                 800
241 ctg ggc acc gtg acc atc ctc tgc att gac ttg ggc act gac atg gtt   2688
242 Leu Gly Thr Val Thr Ile Leu Cys Ile Asp Leu Gly Thr Asp Met Val
243                 805                 810                 815
245 ccc gcc atc tct ctg gct tat gaa cag gct gaa agt gac atc atg aag   2736
246 Pro Ala Ile Ser Leu Ala Tyr Glu Gln Ala Glu Ser Asp Ile Met Lys
247                 820                 825                 830
249 agg cag ccc aga aat ccc aaa acg gac aag ctt gtg aac gag cgt ctg   2784
250 Arg Gln Pro Arg Asn Pro Lys Thr Asp Lys Leu Val Asn Glu Arg Leu
251     835                 840                 845
253 atc agc atg gcc tat gga cag atc ggt atg atc cag gcc ctg gga ggt   2832
254 Ile Ser Met Ala Tyr Gly Gln Ile Gly Met Ile Gln Ala Leu Gly Gly
255 850                 855                 860                 865
257 ttc ttc act tat ttt gtg att ctg gct gag aac ggt ttc ctg ccc ttt   2880
258 Phe Phe Thr Tyr Phe Val Ile Leu Ala Glu Asn Gly Phe Leu Pro Phe
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259               870              875              880
761  cac ctg ttg ggc atc cga gag acc tgg gat gac cgc tgg atc aat gat   2928
762  His Leu Leu Gly Ile Arg Glu Thr Trp Asp Asp Arg Trp Ile Asn Asp
763               885              890              895
765  gtc gag gac agc tac ggg cag cag tgg acc tac gag cag agg aag att   2976
766  Val Glu Asp Ser Tyr Gly Gln Gln Trp Thr Tyr Glu Gln Arg Lys Ile
767               900              905              910
769  gtg gag ttc acc tgc cac acg gcc ttc ttt gtc agt atc gtg gta gtg   3024
770  Val Glu Phe Thr Cys His Thr Ala Phe Phe Val Ser Ile Val Val Val
771      915              920              925
773  cag tgg gct gac ttg gtc atc tgc aag acc aga agg aat tct gtc ttc   3072
774  Gln Trp Ala Asp Leu Val Ile Cys Lys Thr Arg Arg Asn Ser Val Phe
775      930              935              940              945
777  cag cag gga atc aag aac aag atc tta ata ttt ggc ctc ttt gaa gag   3120
778  Gln Gln Gly Met Lys Asn Lys Ile Leu Ile Phe Gly Leu Phe Glu Glu
779               950              955              960
781  aca gct ctt gct gtt ttc ctc tcc tac tgc cct ggc atg ggt gca gcc   3168
782  Thr Ala Leu Ala Ala Phe Leu Ser Tyr Cys Pro Gly Met Gly Ala Ala
783               965              970              975
785  ctt agg atg tat ccc ctc aaa cct act tgg tgg ttc tgt gcc ttc ccc   3216
786  Leu Arg Met Tyr Pro Leu Lys Pro Thr Trp Trp Phe Cys Ala Phe Pro
787      980              985              990
789  tac tcc ctt ctc atc ttt gtg tat gac gag gtg cgg aag ctc atc atc   3264
790  Tyr Ser Leu Leu Ile Phe Val Tyr Asp Glu Val Arg Lys Leu Ile Ile
791      995              1000             1005
793  agg cga agc cct ggg ggc tgg gtg gag aag gaa acc tac tac tag       3309
794  Arg Arg Arg Pro Gly Gly Trp Val Glu Lys Glu Thr Tyr Tyr  *
795      1010             1015             1020
797  cccactgcc tggaccggt ggaaaattgt gccacacact gaacctaccc ctacccccc   3369
798  ttcgtgtact tcaagtcttg gagccggaa ctctaccctg gtaggaaagc accaaagcat   3429
799  gtgggtgatcc agaagtcctg gaatgaagca tgtagctgta atgggggcg gcgggagggc   3489
800  tgccgtaaa acaccctgga cggcacgac agcgggaag gttatatgt gccttttgt     3549
801  ttttgtaaaa aagcagaacc tggaaagact gaaagattac gttttatatc tggatttta   3609
802  caaataaaaa tgcctattat aacggaa                                     3636
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804  <211> LENGTH: 1023
806  <212> TYPE: PRT
807  <213> ORGANISM: Rattus norvegicus
808  <400> SEQUENCE: 2
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812  Glu His Gly Asp Lys Lys Ser Lys Lys Ala Lys Lys Glu Arg Asp Met
813               20                   25                   30
814  Asp Glu Leu Lys Lys Glu Val Ser Met Asp Asp His Lys Leu Ser Leu
815      35                   40                   45
816  Asp Glu Leu His Arg Lys Tyr Gly Thr Asp Leu Ser Arg Gly Leu Thr
817      50                   55                   60
818  Pro Ala Arg Ala Ala Glu Ile Leu Ala Arg Asp Gly Pro Asn Ala Leu
819  65                   70                   75                   80
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VERIFICATION SUMMARY

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